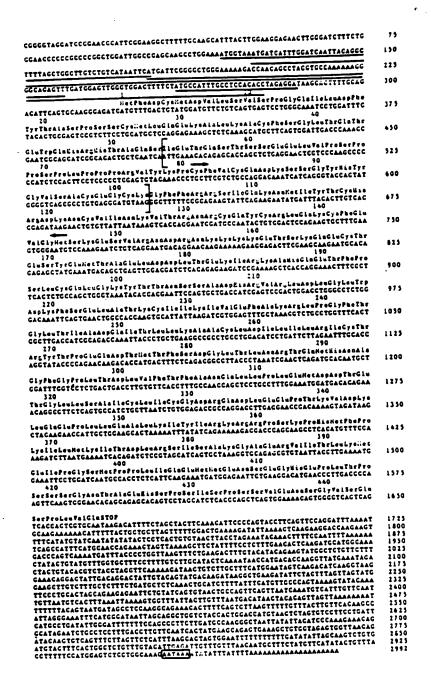


FIGURE 1



a b c d e f g h i j k

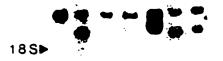
28S

18S



a b c d e f g

28S▶



DODO CONTRUL

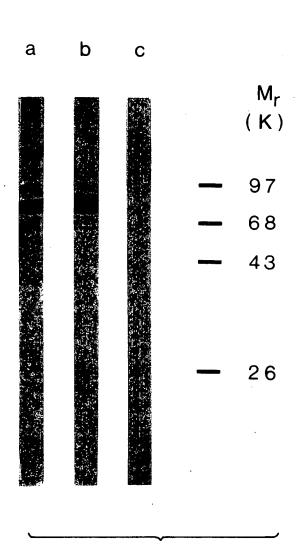


FIG. 5

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81 102 185 568 421	GPVOODKSGOVHYOUS ACTOCROFFRANTIOKNNIYITCHRDKNCYINKVIRNRCOYCRIQKCFEVGHSKESVRNDRNKIKKETSKQECTESY	hap hcenta nER rPR nGR
172 204 285 666 519	EHTAELDDLTEKIBKAHQET	hap hcerbA nEA r PR nGR
259 305 384 753 601	LDIILILRICTRYTPEQDTMTFSDCEITUMRIAPHNAGFGPLTDLVFTFANQLLPLEMDDTETGLUSAIGLICGDRQDIEEPTKVÜÖKLGEPLL MEINSLRAAVRYDPESETITLNGEHAVIRMOGLKNGGLOVSDAIFDLGMSLSSFNLDDTEVALUGAVELHSSGRRCLACVERIEKYQDSEL LEILMIGENWRSDEHPVKLLFAPNILLIDURMOGKCVEGNVE-IBDNLLATSSFRHMNLGGEFVGLRSIILLMSSTAKSLLEKBLIHNHNVLD MSLMVFGLOMRSYKHVSGQMLYFAPDLIILNE-QRHKESSFYSLCLTMWQIPQEFVKLQVSQEEFLOOMKVLLLLNTIPLEGLKSGQELFIERRSSYI MSLMVFGLOMRSYKHVSGQMLYFAPDLIILNE-QRHKESSFYSLCLTMWQIPQEFVKLQVSQEEFLOOMKVLLLLNTIPLEGLKSQELFIEIRRIYI	hap heefbA r P.B nGA
350 396 4 81 847 695	EALKIYIRAMRPSKPHMFPKILMKIJDURSISAKGAERVIJLKHEIPGSH-PPLIQEMMENSEGHEPLTPSSSGNTAEHSPSISPSSVENSGVSGSPLVQ** LAFEHYINYMKHHVTHFWPKLLMKVTDLRHIGACHASRFLHHKVECPTELLPPLFLEVFD*** KITDTLJIHLHAKAGLTLQQQHQRIJACLLIISHIRHMSNKGHEHLYSMKCKNVVPLYDLLIDD*** RELIKAJICLRQCKVVSSSQRFYQLTKILUDNHHDLVKQLHLYCHNTFIQSRALSVEFPEMMSDVIAAQLPKILACHVKPLLFHKK*** KELIKAJICLRQKGVVSSSQRFYQLTKILUDNHHDLVKQLHLYCLNTFIQSRALSVEFPEMMSDVIAAQLPKILACHVKPLKFHQK***	hap hc-erbA hER r PR hGR
583	YIIGEAEGFPATV***	:

	hap	A B   ∴ C ∴	196 D	448 E · · · · · · · · ·
	hc-erbA	102 169	241	456 38 ::::::
	hER	185 250  ∷59∷	319	505 22::::::::
rPR		568 633 ∷42∷	688	930
hGR	1	421 486	536	777 .16 :

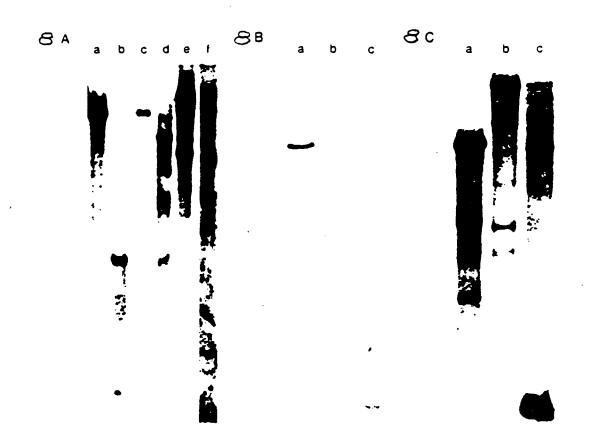
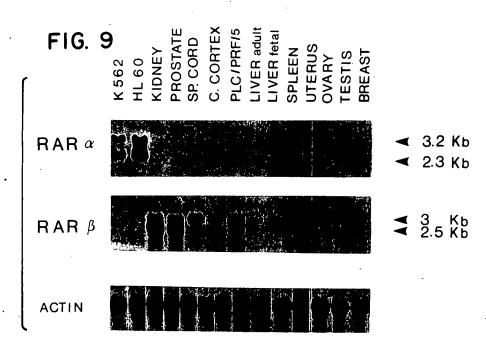
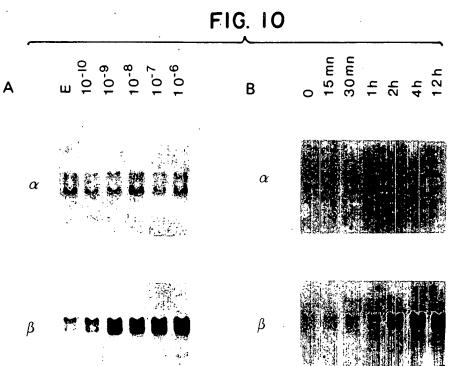


FIGURE 8





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FIG. 12

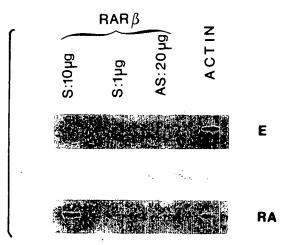
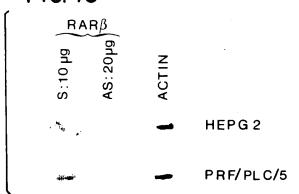
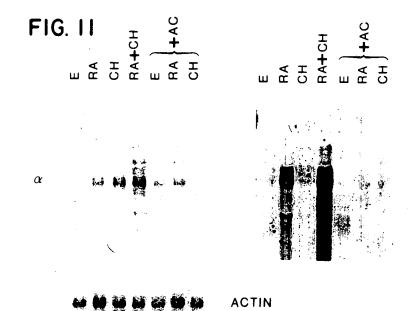
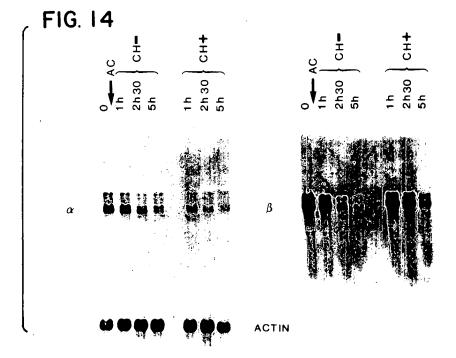


FIG. 13

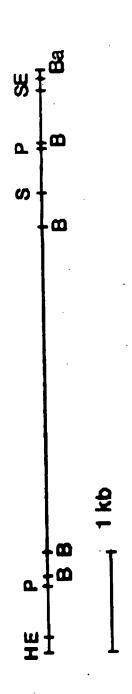


10





10 20 30 40 50 50 70 70 CCCATGCGAGCGATGCCGAGCGAGCGATTGTCTGGGCACCGT 8 SP 12 86 8 A N I FOX I SFANI



H: Hind III, E: EcoR I, P: Pvu II, B: Bgi II, S: Sme I, Ba: BamH I. No Kpn I, Sec I, Sph I, Xho I are found in this DNA insert FIGURE 16

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